

Abstract

The present invention concerns methods for measuring drug resistance by correlating genotypic information with phenotypic profiles. In one embodiment, a method for interpreting genotypic information is described wherein a genetic code is generated from a patient sample, a list of mutations known or suspect to play a role in the development of resistance to one or more drugs is obtained from the generated genetic code, a genotype database is interrogated for previous samples with similar mutations relating to said one or more drugs, a phenotype for said sample is located in a phenotype database, the mean change in inhibition is determined based on all the examples located in said phenotype database, a distribution of sensitivities of one or more drugs suitable for treating a specific indication is determined.